

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/824,575A
Source: 1600
Date Processed by STIC: 1/11/05

ENTERED

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NOV 14 2005

TECH CENTER 1600/2900



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/824,575A

DATE: 01/11/2005

TIME: 17:44:11

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\01112005\I824575A.raw

4 <110> APPLICANT: BEASLEY, Ellen M. et al
 6 <120> TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 7 NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
 8 AND USES THEREOF
 10 <130> FILE REFERENCE: CL000998
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/824,575A
 C--> 12 <141> CURRENT FILING DATE: 2001-04-03
 12 <160> NUMBER OF SEQ ID NOS: 4
 14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 3487
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Human
 21 <400> SEQUENCE: 1
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 23 aggcacccgc ccgcaccatt tacctaacc aaccgcattt caacaatcc cgcgacaacc 120
 24 ggatcgtac ggccaagtac agcgtgttga catttttacc tcgattcttg tatgagcaga 180
 25 tttagaagagc tgctaatgcc ttctttctct tcattgcctt attacagcaa attccagatg 240
 26 tatctccaac aggaagat accaccctgg tgccattgtat cattatTTTA acaattgcag 300
 27 gcatcaaaga gattgttagaa gatTTTAAGC gacacaaggc agacaatgca gttAACAAAA 360
 28 agaaaaacaat agtgttaaga aatggtatgt ggcataccat tatgtggaaa gaggtggcag 420
 29 tgggagacat tgtgaaggc gtcataatgggc agtatcttcc agcagatgtg gtcctgctgt 480
 30 catccagtga acctcaggca atgtgtttagt ttgaaacagc taatctggat gggagacga 540
 31 accttaaaat acgtcagggt ttgagtacca ctgctgacat gcaaacaatgt gaaggctcga 600
 32 tgaagttatc tggaaactata gagtgtgaag ggcccaaccg ccacctcttat gacttcactg 660
 33 gaaacttgaa cttagatggg aaaaggcttg ttgccttgg gcctgaccag atcttattaa 720
 34 gaggtacaca gcttagaaat actcagtggg tctttggcat agttgtttat actggacacg 780
 35 acacccaaact catgcagaat tcaacccaaag cgcctctcaa gagatcaaatt gttgagaagg 840
 36 tgactaacgt gcagatccctg gtgtgtttt gcatcctt ggtcatggcc ttggtgagct 900
 37 cggcgggggc cctgtactgg aacaggcttc atggtaaaaa gaactggatc atcaagaaga 960
 38 tggacaccac ctcagataat ttggataca acctactgac gttcatcata ttatacaaca 1020
 39 atcttattcc catcagtctg ttggtgactc ttgaggttgc gaagtataact caagccctt 1080
 40 tcataaactg ggacacagat atgttattata taggaatga cactcctgcc atggccagga 1140
 41 catcaaacct taatgaagag ctggggcagg tggaaatatct cttttctgac aagactggaa 1200
 42 cgcttacatg caatatcatg aactttaaga agtgcagcat tgccggagta acttatggtc 1260
 43 acttcccaga attggcaaga gagccgtctt cagatgactt ctgtcggtatg cctcctccct 1320
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 45 ccacagcccc ttgcattcag gagttcctca cccttctggc cgtgtgccac acggttggc 1440
 46 ctgagaagga tggagataac atcatctacc aggcccttcc cccagatgaa gctgcttgg 1500
 47 tggaaaggagc taaaaagctg ggctttgtct tcacagccag aacaccatcc tcagtcata 1560
 48 tagaagcgat gggacaggaa caaacatttgc gatccttaa tggctctggaa ttttcttagt 1620
 49 acagaaaaag aatgtctgta attgttcgaa ctccctcagg acgacttcgg ctttactgta 1680
 50 aaggggctga taatgtgatt ttggagagac ttcaaaaat atggaggaaa 1740

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51 cattatgcc a tctggaaatac tttgccacgg aaggcttgcg gactcttgt gtggcttatg 1800
 52 ctgatcttc tgagaatgag tatgaggagt ggctgaaagt ctatcaggaa gccagcacca 1860
 53 tattgaagga cagagctcaa cggttggaa agtgttacga gatcatttag aagaatttg 1920
 54 tgctacttgg agccacagcc atagaagatc gccttcaagc aggagttcca gaaaccatcg 1980
 55 caacactgtt gaaggcagaa attaaaatat gggtgttgc aggagacaaa caagaaactg 2040
 56 cgattaatat agggtattcc tgccgattgg tatcgcagaa tatggccctt atcctattga 2100
 57 aggaggactc tttggatgcc acaaggcag ccattactca gcactgact gaccttggg 2160
 58 atttgctggg caaggaaaat gacgtggccc tcatacatcga tggccacacc ctgaagtacg 2220
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 60 tatgctgcag agtgtctcct ctgcagaagt ctgagatagt gatgtggg aagaagcggg 2340
 61 tgaaggccat caccctcgcc atcggagacg ggcacacga tgcggggatg atccagacag 2400
 62 cccacgtggg tgtggaaatc agtggaaatc aaggcatgca gccaccaac aactcggatt 2460
 63 acgccccatcgc acagtttcc tacttagaga agcttctgtt gttcatgca gcctggagct 2520
 64 acaaccgggt gaccaagtgc atcttgcact gttctataa gacgtggc ctgtatatta 2580
 65 ttgagctttt gttcgcttt gtaatggat tttctggca gattttattt gacgttgg 2640
 66 gcatcggcct gtacaatgtg atttcaccc ctttggccctt cttcaactctg ggaatcttt 2700
 67 agaggtcttgc cactcaggag agcatgctca ggtttccca gctctacaaa atcaccac 2760
 68 atggcgaagg cttcaacaca aagggtttctt ggggtcactg catcaacgcc ttggccact 2820
 69 ccctccatcctt ctctgtttt cccatgaaag ctctggagca tgatactgtg ttgacaagt 2880
 70 gtcatgttac cgactattta ttgttggaa atatttttta cacatatgtt gttttactg 2940
 71 tttgtctgaa agctggggg gagaccacaa cttggactaa attcagtcat ctggctgtct 3000
 72 ggggaagcat gctgacctgg ctgggtttt ttggcatcta ctcgaccatc tggccacca 3060
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 74 gttgggatt atttctgtt cctactgcct gtttatttga agatgtggca tggagagcag 3180
 75 ccaagcacac ctgcaaaaag acattgcccgg aggaggtgca ggagctggaa accaagtctc 3240
 76 gagtcctggg aaaagcggtg ctgcgggata gcaatggaaa gaggtgaaac gagcgcgacc 3300
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 84 <212> TYPE: PRT
 85 <213> ORGANISM: Human
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 90 Thr Ile Tyr Leu Asn Gln Pro His Leu Asn Lys Phe Arg Asp Asn Arg
 91 20 25 30
 92 Ile Ser Thr Ala Lys Tyr Ser Val Leu Thr Phe Leu Pro Arg Phe Leu
 93 35 40 45
 94 Tyr Glu Gln Ile Arg Arg Ala Ala Asn Ala Phe Phe Leu Phe Ile Ala
 95 50 55 60
 96 Leu Leu Gln Gln Ile Pro Asp Val Ser Pro Thr Gly Arg Tyr Thr Thr
 97 65 70 75 80
 98 Leu Val Pro Leu Ile Ile Leu Thr Ile Ala Gly Ile Lys Glu Ile
 99 85 90 95
 100 Val Glu Asp Phe Lys Arg His Lys Ala Asp Asn Ala Val Asn Lys Lys
 101 100 105 110

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102 Lys Thr Ile Val Leu Arg Asn Gly Met Trp His Thr Ile Met Trp Lys
103      115          120          125
104 Glu Val Ala Val Gly Asp Ile Val Lys Val Val Asn Gly Gln Tyr Leu
105      130          135          140
106 Pro Ala Asp Val Val Leu Leu Ser Ser Ser Glu Pro Gln Ala Met Cys
107      145          150          155          160
108 Tyr Val Glu Thr Ala Asn Leu Asp Gly Glu Thr Asn Leu Lys Ile Arg
109      165          170          175
110 Gln Gly Leu Ser His Thr Ala Asp Met Gln Thr Arg Glu Val Leu Met
111      180          185          190
112 Lys Leu Ser Gly Thr Ile Glu Cys Glu Gly Pro Asn Arg His Leu Tyr
113      195          200          205
114 Asp Phe Thr Gly Asn Leu Asn Leu Asp Gly Lys Ser Leu Val Ala Leu
115      210          215          220
116 Gly Pro Asp Gln Ile Leu Leu Arg Gly Thr Gln Leu Arg Asn Thr Gln
117      225          230          235          240
118 Trp Val Phe Gly Ile Val Val Tyr Thr Gly His Asp Thr Lys Leu Met
119      245          250          255
120 Gln Asn Ser Thr Lys Ala Pro Leu Lys Arg Ser Asn Val Glu Lys Val
121      260          265          270
122 Thr Asn Val Gln Ile Leu Val Leu Phe Gly Ile Leu Leu Val Met Ala
123      275          280          285
124 Leu Val Ser Ser Ala Gly Ala Leu Tyr Trp Asn Arg Ser His Gly Glu
125      290          295          300
126 Lys Asn Trp Tyr Ile Lys Lys Met Asp Thr Thr Ser Asp Asn Phe Gly
127      305          310          315          320
128 Tyr Asn Leu Leu Thr Phe Ile Ile Leu Tyr Asn Asn Leu Ile Pro Ile
129      325          330          335
130 Ser Leu Leu Val Thr Leu Glu Val Val Lys Tyr Thr Gln Ala Leu Phe
131      340          345          350
132 Ile Asn Trp Asp Thr Asp Met Tyr Tyr Ile Gly Asn Asp Thr Pro Ala
133      355          360          365
134 Met Ala Arg Thr Ser Asn Leu Asn Glu Glu Leu Gly Gln Val Lys Tyr
135      370          375          380
136 Leu Phe Ser Asp Lys Thr Gly Thr Leu Thr Cys Asn Ile Met Asn Phe
137      385          390          395          400
138 Lys Lys Cys Ser Ile Ala Gly Val Thr Tyr Gly His Phe Pro Glu Leu
139      405          410          415
140 Ala Arg Glu Pro Ser Ser Asp Asp Phe Cys Arg Met Pro Pro Pro Cys
141      420          425          430
142 Ser Asp Ser Cys Asp Phe Asp Asp Pro Arg Leu Leu Arg Asn Ile Glu
143      435          440          445
144 Asp Arg His Pro Thr Ala Pro Cys Ile Gln Glu Phe Leu Thr Leu Leu
145      450          455          460
146 Ala Val Cys His Thr Val Val Pro Glu Lys Asp Gly Asp Asn Ile Ile
147      465          470          475          480
148 Tyr Gln Ala Ser Ser Pro Asp Glu Ala Ala Leu Val Lys Gly Ala Lys
149      485          490          495
150 Lys Leu Gly Phe Val Phe Thr Ala Arg Thr Pro Phe Ser Val Ile Ile

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151	500	505	510
152	Glu Ala Met Gly Gln Glu Gln Thr Phe Gly Ile Leu Asn Val Leu Glu		
153	515	520	525
154	Phe Ser Ser Asp Arg Lys Arg Met Ser Val Ile Val Arg Thr Pro Ser		
155	530	535	540
156	Gly Arg Leu Arg Leu Tyr Cys Lys Gly Ala Asp Asn Val Ile Phe Glu		
157	545	550	555
158	Arg Leu Ser Lys Asp Ser Lys Tyr Met Glu Glu Thr Leu Cys His Leu		
159	565	570	575
160	Glu Tyr Phe Ala Thr Glu Gly Leu Arg Thr Leu Cys Val Ala Tyr Ala		
161	580	585	590
162	Asp Leu Ser Glu Asn Glu Tyr Glu Glu Trp Leu Lys Val Tyr Gln Glu		
163	595	600	605
164	Ala Ser Thr Ile Leu Lys Asp Arg Ala Gln Arg Leu Glu Glu Cys Tyr		
165	610	615	620
166	Glu Ile Ile Glu Lys Asn Leu Leu Leu Gly Ala Thr Ala Ile Glu		
167	625	630	635
168	640		
169	Asp Arg Leu Gln Ala Gly Val Pro Glu Thr Ile Ala Thr Leu Leu Lys		
170	645	650	655
171	Ala Glu Ile Lys Ile Trp Val Leu Thr Gly Asp Lys Gln Glu Thr Ala		
172	660	665	670
173	Ile Asn Ile Gly Tyr Ser Cys Arg Leu Val Ser Gln Asn Met Ala Leu		
174	675	680	685
175	Ile Leu Leu Lys Glu Asp Ser Leu Asp Ala Thr Arg Ala Ala Ile Thr		
176	690	695	700
177	Gln His Cys Thr Asp Leu Gly Asn Leu Leu Gly Lys Glu Asn Asp Val		
178	705	710	715
179	720		
180	Ala Leu Ile Ile Asp Gly His Thr Leu Lys Tyr Ala Leu Ser Phe Glu		
181	725	730	735
182	Val Arg Arg Ser Phe Leu Asp Leu Ala Leu Ser Cys Lys Ala Val Ile		
183	740	745	750
184	Cys Cys Arg Val Ser Pro Leu Gln Lys Ser Glu Ile Val Asp Val Val		
185	755	760	765
186	Lys Lys Arg Val Lys Ala Ile Thr Leu Ala Ile Gly Asp Gly Ala Asn		
187	770	775	780
188	Asp Val Gly Met Ile Gln Thr Ala His Val Gly Val Gly Ile Ser Gly		
189	785	790	795
190	800		
191	Asn Glu Gly Met Gln Ala Thr Asn Asn Ser Asp Tyr Ala Ile Ala Gln		
192	805	810	815
193	Phe Ser Tyr Leu Glu Lys Leu Leu Leu Val His Gly Ala Trp Ser Tyr		
194	820	825	830
195	Asn Arg Val Thr Lys Cys Ile Leu Tyr Cys Phe Tyr Lys Asn Val Val		
196	835	840	845
197	Leu Tyr Ile Ile Glu Leu Trp Phe Ala Phe Val Asn Gly Phe Ser Gly		
198	850	855	860
199	Gln Ile Leu Phe Glu Arg Trp Cys Ile Gly Leu Tyr Asn Val Ile Phe		
	865	870	875
	880		
	Thr Ala Leu Pro Pro Phe Thr Leu Gly Ile Phe Glu Arg Ser Cys Thr		
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200 Gln Glu Ser Met Leu Arg Phe Pro Gln Leu Tyr Lys Ile Thr Gln Asn
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202 Gly Glu Gly Phe Asn Thr Lys Val Phe Trp Gly His Cys Ile Asn Ala
203 915 920 925
204 Leu Val His Ser Leu Ile Leu Phe Trp Phe Pro Met Lys Ala Leu Glu
205 930 935 940
206 His Asp Thr Val Leu Thr Ser Gly His Ala Thr Asp Tyr Leu Phe Val
207 945 950 955 960
208 Gly Asn Ile Val Tyr Thr Val Val Val Thr Val Cys Leu Lys Ala
209 965 970 975
210 Gly Leu Glu Thr Thr Ala Trp Thr Lys Phe Ser His Leu Ala Val Trp
211 980 985 990
212 Gly Ser Met Leu Thr Trp Leu Val Phe Phe Gly Ile Tyr Ser Thr Ile
213 995 1000 1005
214 Trp Pro Thr Ile Pro Ile Ala Pro Asp Met Arg Gly Gln Ala Thr Met
215 1010 1015 1020
216 Val Leu Ser Ser Ala His Phe Trp Leu Gly Leu Phe Leu Val Pro Thr
217 1025 1030 1035 1040
218 Ala Cys Leu Ile Glu Asp Val Ala Trp Arg Ala Ala Lys His Thr Cys
219 1045 1050 1055
220 Lys Lys Thr Leu Pro Glu Glu Val Gln Glu Leu Glu Thr Lys Ser Arg
221 1060 1065 1070
222 Val Leu Gly Lys Ala Val Leu Arg Asp Ser Asn Gly Lys Arg Leu Asn
223 1075 1080 1085
224 Glu Arg Asp Arg Leu Ile Lys Arg Pro Gly Arg Lys Thr Pro Pro Thr
225 1090 1095 1100
226 Leu Phe Arg Gly Ser Ser Leu Gln Gln Gly Val Pro His Gly Tyr Ala
227 1105 1110 1115 1120
228 Phe Ser Gln Glu His Gly Ala Val Ser Gln Glu Glu Val Ile Arg
229 1125 1130 1135
230 Ala Tyr Asp Thr Thr Lys Lys Ser Arg Lys Lys
231 1140 1145
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 559686
236 <212> TYPE: DNA
237 <213> ORGANISM: Human
239 <220> FEATURE:
240 <221> NAME/KEY: misc_feature
241 <222> LOCATION: (1)...(559686)
242 <223> OTHER INFORMATION: n = A,T,C or G
244 <400> SEQUENCE: 3
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247 aggaacctga tcttcgttt ttgtgttctc agcggcatct aacaagtgtat cctgactggg 180
248 tgctcatcag catcaacttag tgatctttag aagaaaaaca cagtgaccac agaatctgag 240
249 agggcagggc ccggaaacta atacattgtg gaagctgcat tggtaataact aatgcacagg 300
250 ggaactgaga gccgcttaggt gagcaatgaa ccacttgac cacgcactgt tcagtgaacc 360
251 cagcctgtcc ctactgtcct ggagcttggg cttctgggtg cagtgagaca gagcatccat 420
252 aaataaaaatc aggtatatgtat gatatctggt actgtggagg aagacaaggc agggttagtg 480

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/11/2005
 PATENT APPLICATION: US/09/824,575A TIME: 17:44:12

Input Set : A:\Seqlist.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:921 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:40560
M:341 Repeated in SeqNo=3